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The figure displays six panels of protein analysis for different regions of the protein. Each panel shows the amino acid sequence, secondary structure (alpha helices and beta strands), solvent accessibility (SS), confidence scores, and disorder predictions.

- Panel 1 (Residues 1-60):** Sequence: MKKLI NDVQDVL DEQLAGLA KAHP S LTLHQDPVYVTRADAPVAGKVALLS GGGSGHEP MH. Secondary structure shows a beta strand (residues 10-25) and a beta sheet (residues 30-45). SS is high (red) for the first 25 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 1-10 and 45-55.
- Panel 2 (Residues 70-120):** Sequence: CGYI GQGMLS GACPGEI FTSPTPDKI FECA MQVDGGEGVLLIIKNYTGDILNFETATELL. Secondary structure shows a beta strand (residues 75-85) and a beta sheet (residues 90-105). SS is high (red) for the first 75 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 75-85 and 105-115.
- Panel 3 (Residues 130-180):** Sequence: HDSGVKVTTVVI DDDVAVKDSL YTAGRRGVANTVLI EKL VGAA AERGDSL DACAE LGRKL. Secondary structure shows a beta strand (residues 135-145) and a beta sheet (residues 150-165). SS is high (red) for the first 135 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 135-145 and 165-175.
- Panel 4 (Residues 190-240):** Sequence: NNQGH SI GI ALGACTVPAAGKPSFTLADNE MFGVGI HGE PGI DR RPFS SLDQTVDEMF D. Secondary structure shows a beta strand (residues 195-205) and a beta sheet (residues 210-225). SS is high (red) for the first 195 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 195-205 and 225-235.
- Panel 5 (Residues 250-300):** Sequence: TLLVNGSYHRTLRFWDYQQGSWQEEQQTQKPLQSGDRVI ALVNNLGATPLSELYGVYNRL. Secondary structure shows a beta strand (residues 255-265) and a beta sheet (residues 270-285). SS is high (red) for the first 255 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 255-265 and 285-295.
- Panel 6 (Residues 310-350):** Sequence: TTRCQQAGLTIERNLIGAYCTSLDMTGFSITLLKVDDETLALWDAPVHTPALNWGK. Secondary structure shows a beta strand (residues 315-325) and a beta sheet (residues 330-345). SS is high (red) for the first 315 residues and lower (green/yellow) for the rest. Disorder is predicted for residues 315-325 and 345-355.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand